



## SEQUENCE LISTING

<110> Palese, Peter  
O'Neill, Robert

<120> IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS  
THAT INHIBIT INTERACTION OF HOST CELL PROTEINS  
AND VIRAL PROTEINS REQUIRED FOR VIRAL REPLICATION

<130> 6923-119

<140> 10/724, 273  
<141> 2003-11-24

<150> 08/444, 994  
<151> 1995-05-19

<150> 08/246, 583  
<151> 1994-05-20

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Pro Gly Lys Glu Asn Phe Arg Leu Lys Ser Tyr Lys Asn Lys Ser Leu
5 10 15

aat ccc gat gag atg cgc agg agg gag gaa gaa gga ctg cag tta 151
Asn Pro Asp Glu Met Arg Arg Arg Glu Glu Gly Leu Gln Leu
20 25 30 35

cga aag cag aaa aga gaa gag cag tta ttc aag cgg aga aat gtt gct 199
Arg Lys Gln Lys Arg Glu Gln Leu Phe Lys Arg Arg Asn Val Ala
40 45 50

aca gca gaa gaa aca gaa gaa gtt atg tca gat gga ggc ttt 247
Thr Ala Glu Glu Thr Glu Glu Val Met Ser Asp Gly Gly Phe
55 60 65

cat gag gct cag att agt aac atg gag atg gca cca ggt ggt gtc atc 295
His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly Gly Val Ile
70 75 80

act tct gac att gag atg ata ttt tcc aaa agc cca gag caa cag 343
Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro Glu Gln Gln
85 90 95

ctt tca gca aca cag aaa ttc agg aag ctg ctt tca aaa gaa cct aac 391
Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys Glu Pro Asn
100 105 110 115

cct cct att gat gaa gtt atc agc aca cca gga gta gtg gcc agg ttt 439
Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val Ala Arg Phe
120 125 130

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Ser Pro Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu Asn Val Leu			
245	250	255	
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260	265	270	275
tgg gcc ctc tca tat cta tca gat gga ccc aat gat aaa att caa gcg		919	
Trp Ala Leu Ser Tyr Leu Ser Asp Gly Pro Asn Asp Lys Ile Gln Ala			
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Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu Leu Met His			
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ctg cag agt tta ttg cat ttg ctg agt agc cca aag gaa tct atc aaa		1111	
Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu Ser Ile Lys			
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Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly Asn Arg Ala			
360	365	370	

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att tta caa act gct gaa ttt cg <sup>g</sup> aca aga aaa gaa gca gct tgg gcc Ile Leu Gln Thr Ala Glu Phe Arg Thr Arg Lys Glu Ala Ala Trp Ala 390	395	400	1255
atc aca aat gca act tct gga gga tca gct gaa cag atc aag tac cta Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile Lys Tyr Leu 405	410	415	1303
gta gaa ctg ggt tgt atc aag ccg ctc tgt gat ctc ctc acg gtc atg Val Glu Leu Gly Cys Ile Lys Pro Leu Cys Asp Leu Leu Thr Val Met 420	425	430	1351
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<213> Homo sapiens

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Asn Val Ala Thr Ala Glu Glu Thr Glu Glu Glu Val Met Ser Asp  
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Gly Gly Phe His Glu Ala Gln Ile Ser Asn Met Glu Met Ala Pro Gly  
65 70 75 80  
Gly Val Ile Thr Ser Asp Met Ile Glu Met Ile Phe Ser Lys Ser Pro  
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Glu Gln Gln Leu Ser Ala Thr Gln Lys Phe Arg Lys Leu Leu Ser Lys  
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Glu Pro Asn Pro Pro Ile Asp Glu Val Ile Ser Thr Pro Gly Val Val  
115 120 125  
Ala Arg Phe Val Glu Phe Leu Lys Arg Lys Glu Asn Cys Ser Leu Gln  
130 135 140  
Phe Glu Ser Ala Trp Val Leu Thr Asn Ile Ala Ser Gly Asn Ser Leu  
145 150 155 160  
Gln Thr Arg Ile Val Ile Gln Ala Arg Ala Val Pro Ile Phe Ile Glu  
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Leu Gly Asn Ile Ala Gly Asp Ser Thr Met Cys Arg Asp Tyr Val Leu  
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Asp Cys Asn Ile Leu Pro Pro Leu Leu Gln Leu Phe Ser Lys Gln Asn  
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Arg Leu Thr Met Thr Arg Asn Ala Val Trp Ala Leu Ser Asn Leu Cys  
225 230 235 240  
Arg Gly Lys Ser Pro Pro Glu Phe Ala Lys Val Ser Pro Cys Leu  
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275 280 285  
Ile Gln Ala Val Ile Asp Ala Gly Val Cys Arg Arg Leu Val Glu Leu  
290 295 300  
Leu Met His Asn Asp Tyr Lys Val Val Ser Pro Ala Leu Arg Ala Val  
305 310 315 320  
Gly Asn Ile Val Thr Gly Asp Asp Ile Gln Thr Gln Val Ile Leu Asn  
325 330 335  
Cys Ser Ala Leu Gln Ser Leu Leu His Leu Leu Ser Ser Pro Lys Glu  
340 345 350  
Ser Ile Lys Lys Glu Ala Cys Trp Thr Ile Ser Asn Ile Thr Ala Gly  
355 360 365  
Asn Arg Ala Gln Ile Gln Thr Val Ile Asp Ala Asn Ile Phe Pro Ala

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Ala Trp Ala Ile Thr Asn Ala Thr Ser Gly Gly Ser Ala Glu Gln Ile		400
405	410	415
Lys Tyr Leu Val Glu Leu Gly Cys Ile Lys Pro Leu Cys Asp Leu Leu		
420	425	430
Thr Val Met Asp Ser Lys Ile Val Gln Val Ala Leu Asn Gly Leu Glu		
435	440	445
Asn Ile Leu Arg Leu Gly Glu Gln Glu Ala Lys Arg Asn Gly Thr Gly		
450	455	460
Ile Asn Pro Tyr Cys Ala Leu Ile Glu Glu Ala Tyr Gly Leu Asp Lys		
465	470	475
Ile Glu Phe Leu Gln Ser His Glu Asn Gln Glu Ile Tyr Gln Lys Ala		
485	490	495
Phe Asp Leu Ile Glu His Tyr Phe Gly Thr Glu Asp Glu Asp Ser Ser		
500	505	510
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Cys Glu Ala Pro Met Glu Gly Phe Gln Leu		
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Gln Ile Leu Ser Arg Glu His Arg Pro Pro Ile Asp Val Val Ile Gln		
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Ala Gly Val Val Pro Arg Leu Val Glu Phe Met Arg Glu Asn Gln Pro		
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Glu Met Leu Gln Leu Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser		
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Gly Thr Ser Ala Gln Thr Lys Val Val Val Asp Ala Asp Ala Val Pro		
165	170	175
Leu Phe Ile Gln Leu Leu Tyr Thr Gly Ser Val Glu Val Lys Glu Gln		
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Ala Ile Trp Ala Leu Gly Asn Val Ala Gly Asp Ser Thr Asp Tyr Arg		
195	200	205
Asp Tyr Val Leu Gln Cys Asn Ala Met Glu Pro Ile Leu Gly Leu Phe		
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Asn Ser Asn Lys Pro Ser Leu Ile Arg Thr Ala Thr Trp Thr Leu Ser		

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Thr	Leu	Val	Asp	Ala	Cys	Trp	Ala	Ile	Ser	Tyr	Leu	Ser	Asp	Gly	Proline
					275				280						285
Gln	Glu	Ala	Ile	Gln	Ala	Val	Ile	Asp	Val	Arg	Ile	Pro	Lys	Arg	Leucine
					290				295						300
Val	Glu	Leu	Leu	Ser	His	Glu	Ser	Thr	Leu	Val	Gln	Thr	Pro	Ala	Leu
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Arg	Ala	Val	Gly	Asn	Ile	Val	Thr	Gly	Asn	Asp	Leu	Gln	Thr	Gln	Valine
					325				330						335
Val	Ile	Asn	Ala	Gly	Val	Leu	Pro	Ala	Leu	Arg	Leu	Leu	Ser	Ser	
					340				345						350
Pro	Lys	Glu	Asn	Ile	Lys	Lys	Glu	Ala	Cys	Trp	Thr	Ile	Ser	Asn	Ile
					355				360						365
Thr	Ala	Gly	Asn	Thr	Glu	Gln	Ile	Gln	Ala	Val	Ile	Asp	Ala	Asn	Leu
					370				375						380
Ile	Pro	Pro	Leu	Val	Lys	Leu	Leu	Glu	Val	Ala	Glu	Tyr	Lys	Thr	Lys
					385				390						400
Lys	Glu	Ala	Cys	Trp	Ala	Ile	Ser	Asn	Ala	Ser	Ser	Gly	Gly	Leu	Gln
					405				410						415
Arg	Pro	Asp	Ile	Ile	Arg	Tyr	Leu	Val	Ser	Gln	Gly	Cys	Ile	Lys	Proline
					420				425						430
Leu	Cys	Asp	Leu	Leu	Glu	Ile	Ala	Asp	Asn	Arg	Ile	Ile	Glu	Val	Threonine
					435				440						445
Leu	Asp	Ala	Leu	Glu	Asn	Ile	Leu	Lys	Met	Gly	Glu	Ala	Asp	Lys	Glutamic acid
					450				455						460
Ala	Arg	Gly	Leu	Asn	Ile	Asn	Glu	Asn	Ala	Asp	Phe	Ile	Glu	Lys	Alanine
					465				470						480
Gly	Gly	Met	Glu	Lys	Ile	Phe	Asn	Cys	Gln	Gln	Asn	Glu	Asn	Asp	Lysine
					485				490						495
Ile	Tyr	Glu	Lys	Ala	Tyr	Lys	Ile	Ile	Glu	Thr	Tyr	Phe	Gly	Glu	Glutamic acid
					500				505						510
Glu	Asp	Ala	Val	Asp	Glu	Thr	Met	Ala	Pro	Gln	Asn	Ala	Gly	Asn	Threonine
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<211> 170

<212> DNA

<213> Homo sapiens

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<223> partial nucleotide sequence of NPI-2

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<212> DNA

<213> Homo sapiens

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 <222> (1)...(1362)

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1	5							10						15		

aag agg aga aat gta agc tca ttt cct gat gat gct act tct ccg ctg 96

Lys	Arg	Arg	Asn	Val	Ser	Ser	Phe	Pro	Asp	Asp	Ala	Thr	Ser	Pro	Leu	
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cag gaa aac cgc aac aac cag ggc act gta aat tgg tct gtt gat gac 144

Gln	Glu	Asn	Arg	Asn	Asn	Gln	Gly	Thr	Val	Asn	Trp	Ser	Val	Asp	Asp	
35								40				45				

att gtc aaa ggc ata aat agc agc aat gtg gaa aat cag ctc caa gct 192

Ile	Val	Lys	Gly	Ile	Asn	Ser	Ser	Asn	Val	Glu	Asn	Gln	Leu	Gln	Ala	
50								55				60				

act caa gct gcc agg aaa cta ctt tcc aga gaa aaa cag ccc ccc ata 240

Thr	Gln	Ala	Ala	Arg	Lys	Leu	Leu	Ser	Arg	Glu	Lys	Gln	Pro	Pro	Ile	
65								70			75		80			

gac aac ata atc cgg gct ggt ttg att ccg aaa ttt gtg tcc ttc ttg 288

Asp	Asn	Ile	Ile	Arg	Ala	Gly	Leu	Ile	Pro	Lys	Phe	Val	Ser	Phe	Leu	
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ggc aga act gat tgt agt ccc att cag ttt gaa tct gct tgg gca ctc 336

Gly	Arg	Thr	Asp	Cys	Ser	Pro	Ile	Gln	Phe	Glu	Ser	Ala	Trp	Ala	Leu	
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Gly	Gly	Ala	Ile	Pro	Ala	Phe	Ile	Ser	Leu	Leu	Ala	Ser	Pro	His	Ala	
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His	Ile	Ser	Glu	Gln	Ala	Val	Trp	Ala	Leu	Gly	Asn	Ile	Ala	Gly	Asp	
145								150			155		160			

ggc tca gtg ttc cga gac ttg gtt att aag tac ggt gca gtt gac cca 528

Gly	Ser	Val	Phe	Arg	Asp	Leu	Val	Ile	Lys	Tyr	Gly	Ala	Val	Asp	Pro	
165								170				175				

ctg ttg gct ctc ctt gca gtt cct gat atg tca tct tta gca tgt ggc 576

Leu	Leu	Ala	Leu	Leu	Ala	Val	Pro	Asp	Met	Ser	Ser	Leu	Ala	Cys	Gly	
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Tyr	Leu	Arg	Asn	Leu	Thr	Trp	Thr	Leu	Ser	Asn	Leu	Cys	Arg	Asn	Lys	
195								200			205					

aat cct gca ccc ccg ata gat gct gtt gag cag att ctt cct acc tta 672

Asn	Pro	Ala	Pro	Pro	Ile	Asp	Ala	Val	Glu	Gln	Ile	Leu	Pro	Thr	Leu	
210								215				220				

gtt	cgg	ctc	ctg	cat	cat	gat	gat	cca	gaa	gtg	tta	gca	gat	acc	tgc	720
Val	Arg	Leu	Leu	His	His	Asp	Asp	Pro	Glu	Val	Leu	Ala	Asp	Thr	Cys	
225						230				235					240	
tgg	gct	att	tcc	tac	ctt	act	gat	ggt	cca	aat	gaa	cga	att	ggc	atg	768
Trp	Ala	Ile	Ser	Tyr	Leu	Thr	Asp	Gly	Pro	Asn	Glu	Arg	Ile	Gly	Met	
						245			250					255		
gtg	gtg	aaa	aca	gga	gtt	gtg	ccc	caa	ctt	gtg	aag	ctt	cta	gga	gct	816
Val	Val	Lys	Thr	Gly	Val	Val	Pro	Gln	Leu	Val	Lys	Leu	Leu	Gly	Ala	
						260			265					270		
tct	gaa	ttg	cca	att	gtg	act	cct	gcc	cta	aga	gcc	ata	ggg	aat	att	864
Ser	Glu	Leu	Pro	Ile	Val	Thr	Pro	Ala	Leu	Arg	Ala	Ile	Gly	Asn	Ile	
						275			280					285		
gtc	act	ggt	aca	gat	gaa	cag	act	cag	gtt	gtg	att	gat	gca	gga	gca	912
Val	Thr	Gly	Thr	Asp	Glu	Gln	Thr	Gln	Val	Val	Ile	Asp	Ala	Gly	Ala	
						290			295					300		
ctc	gcc	gtc	ttt	ccc	agc	ctg	ctc	acc	aac	ccc	aaa	act	aac	att	cag	960
Leu	Ala	Val	Phe	Pro	Ser	Leu	Leu	Thr	Asn	Pro	Lys	Thr	Asn	Ile	Gln	
						305			310			315		320		
aag	gaa	gct	acg	tgg	aca	atg	tca	aac	atc	aca	gcc	gac	cgc	cag	gac	1008
Lys	Glu	Ala	Thr	Trp	Thr	Met	Ser	Asn	Ile	Thr	Ala	Gly	Arg	Gln	Asp	
						325			330					335		
cag	ata	cag	caa	gtt	gtg	aat	cat	gga	tta	gtc	cca	ttc	ctt	gtc	agt	1056
Gln	Ile	Gln	Gln	Val	Val	Asn	His	Gly	Leu	Val	Pro	Phe	Leu	Val	Ser	
						340			345					350		
gtt	ctc	tct	aag	gca	gat	ttt	aag	aca	caa	aag	gaa	gct	gtg	tgg	gcc	1104
Val	Leu	Ser	Lys	Ala	Asp	Phe	Lys	Thr	Gln	Lys	Glu	Ala	Val	Trp	Ala	
						355			360			365				
gtg	acc	aac	tat	acc	agt	ggt	gga	aca	gtt	gaa	cag	att	gtg	tac	ctt	1152
Val	Thr	Asn	Tyr	Thr	Ser	Gly	Gly	Thr	Val	Glu	Gln	Ile	Val	Tyr	Leu	
						370			375			380				
gtt	cac	tgt	ggc	ata	ata	gaa	ccg	ttg	atg	aac	ctc	tta	act	gca	aaa	1200
Val	His	Cys	Gly	Ile	Ile	Glu	Pro	Leu	Met	Asn	Leu	Leu	Thr	Ala	Lys	
						385			390			395		400		
gat	acc	aag	att	att	ctg	gtt	atc	ctg	gat	gcc	att	tca	aat	atc	ttt	1248
Asp	Thr	Lys	Ile	Ile	Leu	Val	Ile	Leu	Asp	Ala	Ile	Ser	Asn	Ile	Phe	
						405			410					415		
cag	gct	gct	gag	aaa	cta	ggt	gaa	act	agc	tgc	ccg	tct	tca	cag	att	1296
Gln	Ala	Ala	Glu	Lys	Leu	Gly	Glu	Thr	Ser	Cys	Pro	Ser	Ser	Gln	Ile	
						420			425					430		
caa	gaa	caa	ggg	aaa	aga	cag	tac	aga	aat	gag	gcg	tcc	gag	gcg	tcg	1344
Gln	Glu	Gln	Gly	Lys	Arg	Gln	Tyr	Arg	Asn	Glu	Ala	Ser	Glu	Ala	Ser	
						435			440			445				
cag	aat	aga	gaa	act	tag	tataatgatt	gaagaatgtg	gaggctttaga							1392	
Gln	Asn	Arg	Glu	Thr	*											
					450											

caaaaattgaa gctctacaaa accatgaaaa tgagtctgtg tataaggctt cguttaagctt 1452  
aattgagaag tatttctctg tagaggaaga ggaagatcaa aacgttgta cagaaactac 1512  
ctctgaaggc tacacttcc aagttcagga tggggctcct gggaccctta acttttagat 1572  
catgtagctg agacataaat ttgttgtgtt ctacgtttgg tattttgtct tattgtttct 1632  
ctactaagaa ctcttctta aatgtggttt gttactgttag cacttttac actgaaacta 1692  
tacctgaaca gttccaactg tacatacata ctgtatgaag cttgtcctct gactagggtt 1752  
ctaatttcta tgtgaaattt cctatcttgc agcatcctgt aaataaacat tcaagtccac 1812  
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<211> 453

<212> PRT

<213> Homo sapiens

<220>

<223> partial nucleotide sequence of NPI-3

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Lys	Arg	Arg	Asn	Val	Ser	Ser	Phe	Pro	Asp	Asp	Ala	Thr	Ser	Pro	Leu
							20		25					30	
Gln	Glu	Asn	Arg	Asn	Asn	Gln	Gly	Thr	Val	Asn	Trp	Ser	Val	Asp	Asp
						35			40				45		
Ile	Val	Lys	Gly	Ile	Asn	Ser	Ser	Asn	Val	Glu	Asn	Gln	Leu	Gln	Ala
						50			55			60			
Thr	Gln	Ala	Ala	Arg	Lys	Leu	Leu	Ser	Arg	Glu	Lys	Gln	Pro	Pro	Ile
						65			70		75			80	
Asp	Asn	Ile	Ile	Arg	Ala	Gly	Leu	Ile	Pro	Lys	Phe	Val	Ser	Phe	Leu
							85			90				95	
Gly	Arg	Thr	Asp	Cys	Ser	Pro	Ile	Gln	Phe	Glu	Ser	Ala	Trp	Ala	Leu
						100			105				110		
Thr	Asn	Ile	Ala	Ser	Gly	Thr	Ser	Glu	Gln	Thr	Lys	Ala	Val	Val	Asp
						115			120			125			
Gly	Gly	Ala	Ile	Pro	Ala	Phe	Ile	Ser	Leu	Leu	Ala	Ser	Pro	His	Ala
						130			135			140			
His	Ile	Ser	Glu	Gln	Ala	Val	Trp	Ala	Leu	Gly	Asn	Ile	Ala	Gly	Asp
						145			150		155			160	
Gly	Ser	Val	Phe	Arg	Asp	Leu	Val	Ile	Lys	Tyr	Gly	Ala	Val	Asp	Pro
						165			170			175			
Leu	Leu	Ala	Leu	Ala	Val	Pro	Asp	Met	Ser	Ser	Leu	Ala	Cys	Gly	
						180			185			190			
Tyr	Leu	Arg	Asn	Leu	Thr	Trp	Thr	Leu	Ser	Asn	Leu	Cys	Arg	Asn	Lys
						195			200			205			
Asn	Pro	Ala	Pro	Pro	Ile	Asp	Ala	Val	Glu	Gln	Ile	Leu	Pro	Thr	Leu
						210			215			220			
Val	Arg	Leu	Leu	His	His	Asp	Asp	Pro	Glu	Val	Leu	Ala	Asp	Thr	Cys
						225			230		235			240	
Trp	Ala	Ile	Ser	Tyr	Leu	Thr	Asp	Gly	Pro	Asn	Glu	Arg	Ile	Gly	Met
						245			250			255			
Val	Val	Lys	Thr	Gly	Val	Val	Pro	Gln	Leu	Val	Lys	Leu	Gly	Ala	
						260			265			270			
Ser	Glu	Leu	Pro	Ile	Val	Thr	Pro	Ala	Leu	Arg	Ala	Ile	Gly	Asn	Ile
						275			280			285			
Val	Thr	Gly	Thr	Asp	Glu	Gln	Thr	Gln	Val	Val	Ile	Asp	Ala	Gly	Ala
						290			295			300			
Leu	Ala	Val	Phe	Pro	Ser	Leu	Leu	Thr	Asn	Pro	Lys	Thr	Asn	Ile	Gln
						305			310		315			320	
Lys	Glu	Ala	Thr	Trp	Thr	Met	Ser	Asn	Ile	Thr	Ala	Gly	Arg	Gln	Asp
						325			330			335			
Gln	Ile	Gln	Gln	Val	Val	Asn	His	Gly	Leu	Val	Pro	Phe	Leu	Val	Ser

340	345	350
Val Leu Ser Lys Ala Asp Phe Lys Thr Gln Lys Glu Ala Val Trp Ala		
355	360	365
Val Thr Asn Tyr Thr Ser Gly Gly Thr Val Glu Gln Ile Val Tyr Leu		
370	375	380
Val His Cys Gly Ile Ile Glu Pro Leu Met Asn Leu Leu Thr Ala Lys		
385	390	395
Asp Thr Lys Ile Ile Leu Val Ile Leu Asp Ala Ile Ser Asn Ile Phe		400
405	410	415
Gln Ala Ala Glu Lys Leu Gly Glu Thr Ser Cys Pro Ser Ser Gln Ile		
420	425	430
Gln Glu Gln Gly Lys Arg Gln Tyr Arg Asn Glu Ala Ser Glu Ala Ser		
435	440	445
Gln Asn Arg Glu Thr		
450		

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<211> 259  
<212> DNA  
<213> Homo sapiens

<220>  
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acttgtttct tcaagctctt ctggcagtga ttctgacagt gaggttgaca aaaagttaag 120  
caggaaaaag caagttgctc cagaaaaacc tgtaaaagaaa caaaagacag gtgagacttc 180  
gagagccctg tcatcttcta aacagagcag cagcagcaga gatgataaca tgtttcagat 240  
tggaaaaatg aggtcagtt 259

<210> 17  
<211> 221  
<212> DNA  
<213> Homo sapiens

<220>  
<223> partial nucleotide sequence of NPI-5

<400> 17  
tgtcgactgt ggcttgagc atccgtcaga agtccagcat gagtgcatcc ctcaggccat 60  
tctggaaatg gatgtcctgt gccaggccaa gtcgggcatg ggaaagacag cagtgtttgt 120  
cttggccaca ctgcaacagc tggagccagt tactggcag gtgtctgtac tggtgatgtg 180  
tcacactcgg gagttggctt ttcagatcat caaggaatat g 221

<210> 18  
<211> 372  
<212> DNA  
<213> Homo sapiens

<220>  
<223> partial nucleotide sequence of NPI-6

<400> 18  
atttgtaaac cccggagcga ggttctgctt acccgaggcc gctgctgtgc ggagaccccc 60  
gggtgaagcc accgtcatca tgtctgacca ggaggcaaaa ccttcaactg aggacttggg 120  
ggataagaag gaaggtgaat atattaaact caaagtcttggacaggata gcagtggat 180  
tcacttcaaa gtgaaaatga caacacatct caagaaactc aaagaatcat actgtcaaag 240  
acagggtgtt ccaatgaatt cactcaggtt tctctttgag ggtcagagaa ttgctgataa 300  
tcataactcca aaagaactgg gaatggagga agaagttgtg attgaagttt atcaggaaca 360

aacgggggggt ca

372

<210> 19

<211> 2675

<212> DNA

<213> Homo sapiens

<220>

<223> nucleotide sequence of NS1I-1

<220>

<221> CDS

<222> (104) ... (2311)

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gcggctctgc ttgttcgtgt gtgtgtcgaa tcaggccta ttc atg ggc tca ccg 115  
Met Gly Ser Pro  
1

ctg agg ttc gac ggg cgg gtg gta ctg gtc acc ggc gcg ggg gca gga 163  
Leu Arg Phe Asp Gly Arg Val Val Leu Val Thr Gly Ala Gly Ala Gly  
5 10 15 20

ttg ggc cga gcc tat gcc ctg gct ttt gca gaa aga gga gcg tta gtt 211  
Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg Gly Ala Leu Val  
25 30 35

gtt gtg aat gat ttg gga ggg gac ttc aaa gga gtt ggt aat ggc tcc 259  
Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val Gly Lys Gly Ser  
40 45 50

tta gct gat aag gtt gtt gaa gaa ata aga agg aga ggt gga aat gca 307  
Leu Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg Gly Gly Lys Ala  
55 60 65

gtg gcc aac tat gat tca gtg gaa gaa gga gag aag gtt gtg aat aca 355  
Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys Val Val Lys Thr  
70 75 80

gcc ctg gat gct ttt gga aga ata gat gtt gtg gtc aac aat gct gga 403  
Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val Asn Asn Ala Gly  
85 90 95 100

att ctg agg gat cat tcc ttt gct agg ata agt gat gaa gac tgg gat 451  
Ile Leu Arg Asp His Ser Phe Ala Arg Ile Ser Asp Glu Asp Trp Asp  
105 110 115

ata atc cac aga gtt cat ttg cgg ggt tca ttc caa gtg aca cgg gca 499  
Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln Val Thr Arg Ala  
120 125 130

gca tgg gaa cac atg aag aaa cag aag tat gga agg att att atg act 547  
Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg Ile Ile Met Thr  
135 140 145

tca tca gct tca gga ata tat ggc aac ttt ggc cag gcc aat tat agt 595  
Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln Ala Asn Tyr Ser  
150 155 160

gct gca aag ttg ggt ctt ctg ggc ctt gca aat tct ctt gca att gaa 643

Ala Ala Lys Leu Gly Leu Leu Gly Leu Ala Asn Ser Leu Ala Ile Glu			
165	170	175	180
ggc agg aaa agc aac att cat tgt aac acc att gct cct aat gcg gga			691
Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile Ala Pro Asn Ala Gly			
185	190	195	
tca cgg atg act cag aca gtt atg cct gaa gat ctt gtg gaa gcc ttg			739
Ser Arg Met Thr Gln Thr Val Met Pro Glu Asp Leu Val Glu Ala Leu			
200	205	210	
aag cca gag tat gtg gca cct ctt gtc ctt tgg ctt tgt cac gag agt			787
Lys Pro Glu Tyr Val Ala Pro Leu Val Leu Trp Leu Cys His Glu Ser			
215	220	225	
tgt gag gag aat ggt ggc ttg ttt gag gtt ggt gca gga tgg att gga			835
Cys Glu Glu Asn Gly Gly Leu Phe Glu Val Gly Ala Gly Trp Ile Gly			
230	235	240	
aaa tta cgc tgg gag cgg act ctt gga gct att gta aga caa aag aat			883
Lys Leu Arg Trp Glu Arg Thr Leu Gly Ala Ile Val Arg Gln Lys Asn			
245	250	255	260
cac cca atg act cct gag gca gtc aag gct aac tgg aag aag atc tgt			931
His Pro Met Thr Pro Glu Ala Val Lys Ala Asn Trp Lys Lys Ile Cys			
265	270	275	
gac ttt gag aat gcc agc aag cct cag agt atc caa gaa tca act ggc			979
Asp Phe Glu Asn Ala Ser Lys Pro Gln Ser Ile Gln Glu Ser Thr Gly			
280	285	290	
agt ata att gaa gtt ctg agt aaa ata gat tca gaa gga gga gtt tca			1027
Ser Ile Ile Glu Val Leu Ser Lys Ile Asp Ser Glu Gly Gly Val Ser			
295	300	305	
gca aat cat act agt cgt gca acg tct aca gca aca tca gga ttt gct			1075
Ala Asn His Thr Ser Arg Ala Thr Ser Thr Ala Thr Ser Gly Phe Ala			
310	315	320	
gga gct att ggc cag aaa ctc cct cca ttt tct tat gct tat acg gaa			1123
Gly Ala Ile Gly Gln Lys Leu Pro Pro Phe Ser Tyr Ala Tyr Thr Glu			
325	330	335	340
ctg gaa gct att atg tat gcc ctt gga gtg gga gcg tca atc aag gat			1171
Leu Glu Ala Ile Met Tyr Ala Leu Gly Val Gly Ala Ser Ile Lys Asp			
345	350	355	
cca aaa gat ttg aaa ttt att tat gaa gga agt tct gat ttc tcc tgt			1219
Pro Lys Asp Leu Lys Phe Ile Tyr Glu Gly Ser Ser Asp Phe Ser Cys			
360	365	370	
ttg ccc acc ttc gga gtt atc ata ggt cag aaa tct atg atg ggt gga			1267
Leu Pro Thr Phe Gly Val Ile Ile Gly Gln Lys Ser Met Met Gly Gly			
375	380	385	
gga tta gca gaa att cct gga ctt tca atc aac ttt gca aag gtt ctt			1315
Gly Leu Ala Glu Ile Pro Gly Leu Ser Ile Asn Phe Ala Lys Val Leu			
390	395	400	
cat gga gag cag tac tta gag tta tat aaa cca ctt ccc aga gca gga			1363
His Gly Glu Gln Tyr Leu Glu Leu Tyr Lys Pro Leu Pro Arg Ala Gly			

405	410	415	420	
aaa tta aaa tgt gaa gca gtt gtc gat gtc cta gat aaa gga tcc Lys Leu Lys Cys Glu Ala Val Val Ala Asp Val Leu Asp Lys Gly Ser 425		430	435	1411
ggt gta gtg att att atg gat gtc tat tct tat tct gag aag gaa ctt Gly Val Val Ile Ile Met Asp Val Tyr Ser Tyr Ser Glu Lys Glu Leu 440		445	450	1459
ata tgc cac aat cag ttc tct ctc ttt ctt gtt ggc tct gga ggc ttt Ile Cys His Asn Gln Phe Ser Leu Phe Leu Val Gly Ser Gly Gly Phe 455	460		465	1507
ggt gga aaa cgg aca tca gac aaa gtc aag gta gct gta gcc ata cct Gly Gly Lys Arg Thr Ser Asp Lys Val Lys Val Ala Val Ala Ile Pro 470	475		480	1555
aat aga cct cct gat gct gta ctt aca gat acc acc tct ctt aat cag Asn Arg Pro Pro Asp Ala Val Leu Thr Asp Thr Thr Ser Leu Asn Gln 485	490	495		1603
gct gct ttg tac cgc ctc agt gga gac cg <sup>g</sup> aat ccc tta cac att gat Ala Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro Leu His Ile Asp 505		510	515	1651
cct aac ttt gct agt cta gca ggt ttt gac aag ccc ata tta cat gga Pro Asn Phe Ala Ser Leu Ala Gly Phe Asp Lys Pro Ile Leu His Gly 520	525		530	1699
tta tgt aca ttt gga ttt tct gcc agg cgt gtg tta cag cag ttt gca Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val Leu Gln Gln Phe Ala 535	540		545	1747
gat aat gat gtg tca aga ttc aag gca gtt aag gct cgt ttt gca aaa Asp Asn Asp Val Ser Arg Phe Lys Ala Val Lys Ala Arg Phe Ala Lys 550	555	560		1795
cca gta tat cca gga caa act cta caa act gag atg tgg aag gaa gga Pro Val Tyr Pro Gly Gln Thr Leu Gln Thr Glu Met Trp Lys Glu Gly 565	570	575	580	1843
aac aga att cat ttt caa acc aag gtc caa gaa act gga gac att gtc Asn Arg Ile His Phe Gln Thr Lys Val Gln Glu Thr Gly Asp Ile Val 585		590	595	1891
att tca aat gca tat gtg gat ctt gca cca aca tct ggt act tca gct Ile Ser Asn Ala Tyr Val Asp Leu Ala Pro Thr Ser Gly Thr Ser Ala 600	605		610	1939
aag aca ccc tct gag ggc ggg aag ctt cag agt acc ttt gta ttt gag Lys Thr Pro Ser Glu Gly Gly Lys Leu Gln Ser Thr Phe Val Phe Glu 615	620		625	1987
gaa ata gga cgc cgc cta aag gat att ggg cct gag gtg gtg aag aaa Glu Ile Gly Arg Arg Leu Lys Asp Ile Gly Pro Glu Val Val Lys Lys 630	635	640		2035
gta aat gct gta ttt gag tgg cat ata acc aaa ggc gga aat att ggg Val Asn Ala Val Phe Glu Trp His Ile Thr Lys Gly Gly Asn Ile Gly 645	650	655	660	2083

gct aag tgg act att gac ctg aaa agt ggt tct gga aaa gtg tac caa 2131  
 Ala Lys Trp Thr Ile Asp Leu Lys Ser Gly Ser Gly Lys Val Tyr Gln  
       665                    670                    675  
  
 ggc cct gca aaa ggt gct gct gat aca aca atc ata ctt tca gat gaa 2179  
 Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile Ile Leu Ser Asp Glu  
       680                    685                    690  
  
 gat ttc atg gag gtg gtc ctg ggc aag ctt gac cct cag aag gca ttc 2227  
 Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp Pro Gln Lys Ala Phe  
       695                    700                    705  
  
 ttt agt ggc agg ctg aag gcc aga ggg aac atc atg ctg agc cag aaa 2275  
 Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile Met Leu Ser Gln Lys  
       710                    715                    720  
  
 ctt cag atg att ctt aaa gac tac gcc aag ctc tga agggcacact 2321  
 Leu Gln Met Ile Leu Lys Asp Tyr Ala Lys Leu \*  
       725                    730                    735  
  
 acactattaa taaaaatgga atcattaaat actctcttca cccaaatatg cttgattatt 2381  
 ctgcaaaagt gattagaact aagatgcagg ggaaattgct taacattttc agatatcaga 2441  
 taactgcaga ttttcatttt ctactaattt ttcatgtatc attattttta caaggaacta 2501  
 tatataagct agcacataat tatkcttctg ttcttagatc tgtatctca taataaaaaaa 2561  
 atttgccca agtcctgttt ccttagaatt tgtagatagca ttgataagtt gaaaggaaaa 2621  
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<220>  
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 Ala Gly Ala Gly Leu Gly Arg Ala Tyr Ala Leu Ala Phe Ala Glu Arg  
   20                      25                      30  
 Gly Ala Leu Val Val Val Asn Asp Leu Gly Gly Asp Phe Lys Gly Val  
   35                      40                      45  
 Gly Lys Gly Ser Leu Ala Asp Lys Val Val Glu Glu Ile Arg Arg Arg  
   50                      55                      60  
 Gly Gly Lys Ala Val Ala Asn Tyr Asp Ser Val Glu Glu Gly Glu Lys  
   65                      70                      75                      80  
 Val Val Lys Thr Ala Leu Asp Ala Phe Gly Arg Ile Asp Val Val Val  
   85                      90                      95  
 Asn Asn Ala Gly Ile Leu Arg Asp His Ser Phe Ala Arg Ile Ser Asp  
   100                    105                      110  
 Glu Asp Trp Asp Ile Ile His Arg Val His Leu Arg Gly Ser Phe Gln  
   115                    120                      125  
 Val Thr Arg Ala Ala Trp Glu His Met Lys Lys Gln Lys Tyr Gly Arg  
   130                    135                      140  
 Ile Ile Met Thr Ser Ser Ala Ser Gly Ile Tyr Gly Asn Phe Gly Gln  
   145                    150                      155                      160  
 Ala Asn Tyr Ser Ala Ala Lys Leu Gly Leu Leu Gly Leu Ala Asn Ser  
   165                    170                      175  
 Leu Ala Ile Glu Gly Arg Lys Ser Asn Ile His Cys Asn Thr Ile Ala  
   180                    185                      190

Pro Asn Ala Gly Ser Arg Met Thr Gln Thr Val Met Pro Glu Asp Leu  
     195                  200                  205  
 Val Glu Ala Leu Lys Pro Glu Tyr Val Ala Pro Leu Val Leu Trp Leu  
     210                  215                  220  
 Cys His Glu Ser Cys Glu Glu Asn Gly Gly Leu Phe Glu Val Gly Ala  
     225                  230                  235                  240  
 Gly Trp Ile Gly Lys Leu Arg Trp Glu Arg Thr Leu Gly Ala Ile Val  
     245                  250                  255  
 Arg Gln Lys Asn His Pro Met Thr Pro Glu Ala Val Lys Ala Asn Trp  
     260                  265                  270  
 Lys Lys Ile Cys Asp Phe Glu Asn Ala Ser Lys Pro Gln Ser Ile Gln  
     275                  280                  285  
 Glu Ser Thr Gly Ser Ile Ile Glu Val Leu Ser Lys Ile Asp Ser Glu  
     290                  295                  300  
 Gly Gly Val Ser Ala Asn His Thr Ser Arg Ala Thr Ser Thr Ala Thr  
     305                  310                  315                  320  
 Ser Gly Phe Ala Gly Ala Ile Gly Gln Lys Leu Pro Pro Phe Ser Tyr  
     325                  330                  335  
 Ala Tyr Thr Glu Leu Glu Ala Ile Met Tyr Ala Leu Gly Val Gly Ala  
     340                  345                  350  
 Ser Ile Lys Asp Pro Lys Asp Leu Lys Phe Ile Tyr Glu Gly Ser Ser  
     355                  360                  365  
 Asp Phe Ser Cys Leu Pro Thr Phe Gly Val Ile Ile Gly Gln Lys Ser  
     370                  375                  380  
 Met Met Gly Gly Leu Ala Glu Ile Pro Gly Leu Ser Ile Asn Phe  
     385                  390                  395                  400  
 Ala Lys Val Leu His Gly Glu Gln Tyr Leu Glu Leu Tyr Lys Pro Leu  
     405                  410                  415  
 Pro Arg Ala Gly Lys Leu Lys Cys Glu Ala Val Val Ala Asp Val Leu  
     420                  425                  430  
 Asp Lys Gly Ser Gly Val Val Ile Ile Met Asp Val Tyr Ser Tyr Ser  
     435                  440                  445  
 Glu Lys Glu Leu Ile Cys His Asn Gln Phe Ser Leu Phe Leu Val Gly  
     450                  455                  460  
 Ser Gly Gly Phe Gly Gly Lys Arg Thr Ser Asp Lys Val Lys Val Ala  
     465                  470                  475                  480  
 Val Ala Ile Pro Asn Arg Pro Pro Asp Ala Val Leu Thr Asp Thr Thr  
     485                  490                  495  
 Ser Leu Asn Gln Ala Ala Leu Tyr Arg Leu Ser Gly Asp Arg Asn Pro  
     500                  505                  510  
 Leu His Ile Asp Pro Asn Phe Ala Ser Leu Ala Gly Phe Asp Lys Pro  
     515                  520                  525  
 Ile Leu His Gly Leu Cys Thr Phe Gly Phe Ser Ala Arg Arg Val Leu  
     530                  535                  540  
 Gln Gln Phe Ala Asp Asn Asp Val Ser Arg Phe Lys Ala Val Lys Ala  
     545                  550                  555                  560  
 Arg Phe Ala Lys Pro Val Tyr Pro Gly Gln Thr Leu Gln Thr Glu Met  
     565                  570                  575  
 Trp Lys Glu Gly Asn Arg Ile His Phe Gln Thr Lys Val Gln Glu Thr  
     580                  585                  590  
 Gly Asp Ile Val Ile Ser Asn Ala Tyr Val Asp Leu Ala Pro Thr Ser  
     595                  600                  605  
 Gly Thr Ser Ala Lys Thr Pro Ser Glu Gly Gly Lys Leu Gln Ser Thr  
     610                  615                  620  
 Phe Val Phe Glu Glu Ile Gly Arg Arg Leu Lys Asp Ile Gly Pro Glu  
     625                  630                  635                  640  
 Val Val Lys Lys Val Asn Ala Val Phe Glu Trp His Ile Thr Lys Gly  
     645                  650                  655  
 Gly Asn Ile Gly Ala Lys Trp Thr Ile Asp Leu Lys Ser Gly Ser Gly  
     660                  665                  670  
 Lys Val Tyr Gln Gly Pro Ala Lys Gly Ala Ala Asp Thr Thr Ile Ile

675                    680                    685  
Leu Ser Asp Glu Asp Phe Met Glu Val Val Leu Gly Lys Leu Asp Pro  
690                    695                    700  
Gln Lys Ala Phe Phe Ser Gly Arg Leu Lys Ala Arg Gly Asn Ile Met  
705                    710                    715                    720  
Leu Ser Gln Lys Leu Gln Met Ile Leu Lys Asp Tyr Ala Lys Leu  
725                    730                    735